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SEQUENCE LISTING

5 <110> UNILEVER PLC
UNILEVER N.V.

<120> ANTIGEN BINDING PROTEINS

10 <130> T3077

<140>
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15 <160> 45

<170> PatentIn Ver. 2.1

<210> 1
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20 <212> PRT
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<223> Description of Artificial Sequence:LINKER

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30 <210> 2
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35 <220>
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45 <210> 3
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65 <400> 4

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2

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Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr
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- 5 <210> 5
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- 10 <220>
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 Ala Asn His Ser Gly Asn Ala Ser
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- 20 <210> 6
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 25 <400> 6
 aggtsmarct gcagsagtcw gg 22
- 30 <210> 7
 <211> 53
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- 35 <220>
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 aacagttaag cttccgcttg cggccgcgga gctggggtct tcgctgtggt gcg 53
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- 45 <210> 8
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- 55 <210> 9
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 60 <400> 9
 ggaattcca atagtggtt agcaatcg 28
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3

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5 <210> 10
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 gaccaacgtg gtcgcctggc aaaacg 26

15 <210> 11
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 20 <400> 11
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25 <210> 12
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 <222> (3)..(110)

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 <222> (117)..(140)

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 <222> (147)..(155)

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 ga gct cat cac aca aac aaa caa aac aaa atg atg ctt ttg caa gcc 47
 Ala His His Thr Asn Lys Gln Asn Lys Met Met Leu Leu Gln Ala
 1 5 10 15

65 ttc ctt ttc ctt ttg gct ggt ttt gca gcc aaa ata tct gcg cag gtg 95
 Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys Ile Ser Ala Gln Val
 20 25 30

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cag ctg cag gag tca taatga ggg acc cag gtc acc gtc tcc tca taatga 146
Gln Leu Gln Glu Ser          Gly Thr Gln Val Thr Val Ser Ser
          35                      40
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ctt aag ctt
Leu Lys Leu
45
155

10
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CONSTRUCT

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Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys Ile Ser Ala Gln Val Gln
          20          25          30

25
Leu Gln Glu Ser
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<210> 15
<211> 8
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CONSTRUCT

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Gly Thr Gln Val Thr Val Ser Ser
      1          5

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<210> 16
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CONSTRUCT

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CONSTRUCT

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5

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 Ala His His Thr Asn Lys Gln Asn Lys Met Met Leu Leu Gln Ala
 1 5 10 15

 ttc ctt ttc ctt ttg gct ggt ttt gca gcc aaa ata tct gcg cag gtg 95
 15 Phe Leu Phe Leu Ala Gly Phe Ala Ala Lys Ile Ser Ala Gln Val
 20 25 30

 cag ctg cag gag tca taatga ggg acc cag gtc acc gtc tcc tca gaa 143
 Gln Leu Gln Glu Ser Gly Thr Gln Val Thr Val Ser Ser Glu
 20 35 40 45

 caa aaa ctc atc tca gaa gag gat ctg aat taatga ctt aag ctt 188
 Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Xaa Lys Leu
 50 55

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 35 Ala His His Thr Asn Lys Gln Asn Lys Met Met Leu Leu Gln Ala Phe
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 Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys Ile Ser Ala Gln Val Gln
 20 25 30
 40 Leu Gln Glu Ser
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45 <210> 19
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 <213> Artificial Sequence
 <223> Description of Artificial Sequence: PLASMID
 50 CONSTRUCT

<400> 19
 Gly Thr Gln Val Thr Val Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu
 1 5 10 15
 55 Asp Leu Xaa

60 <210> 20
 <211> 3
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 CONSTRUCT
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<400> 20
Xaa Lys Leu
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5

<210> 21
<211> 342
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<223> Description of Artificial Sequence: PLASMID
CONSTRUCT

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Gln Val Gln Leu Ser Cys Ala Ala Ser Gly Lys Leu Val Gln Ala Gly Glu
1 5 10 15

25

tct ctg aaa ctc tcc tgt gca gcc tct gga aac acc ttc agt ggc ggc 96
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly Gly
20 25 30

30

ttc atg ggc tgg tac cgc cag gct cca ggg aag cag cgc gag ttg gtc 144
Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

35

gca acc att aat agt aga ggt atc aca aac tat gca gac ttc gtg aag 192
Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val Lys
50 55 60

40

ggc cga ttc acc atc tcc aga gac aat gcc aag aag aca gtg tat ttg 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu
65 70 75 80

40

gaa atg aac agc ctg gaa cct gaa gac acg gcc gtt tat tac tgt tac 288
Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
85 90 95

45

act cac tac ttc aga tcc tac tgg ggt cag ggg acc cag gtc acc gtc 336
Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
100 105 110

50

tcc tca 342
Ser Ser

55

<210> 22
<211> 114
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: PLASMID
CONSTRUCT

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
1 5 10 15

65

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly Gly
20 25 30

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Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45
 5 Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu
 65 70 75 80
 10 Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
 85 90 95
 Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
 100 105 110
 15 Ser Ser

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 20 <211> 351
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 25 <223> Description of Artificial Sequence: PLASMID
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 <220>
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 30 <222> (1)..(351)

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 35 1 5 10 15

 tct ctg aga ctc tcc tgt gca gcc tct gga cgc acc ggc agt acg tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr
 20 25 30
 40 gac atg ggc tgg ttc cgc cag gct cca ggg aag gag cgt gag tct gta 144
 Asp Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val
 35 40 45
 45 gca gct att aac tgg gat agt gcg cgc aca tac tat gca agc tcc gtg 192
 Ala Ala Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val
 50 55 60
 50 agg ggc cga ttc acc atc tcc aga gac aac gcc aag aag acg gtg tat 240
 Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
 65 70 75 80
 ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt tat acc tgt 288
 Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys
 55 85 90 95
 ggc gcg ggg gaa ggt ggt act tgg gac tcc tgg ggc cag ggg acc cag 336
 Gly Ala Gly Glu Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln
 100 105 110
 60 gtc acc gtc tcc tca 351
 Val Thr Val Ser Ser
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     1          5          10          15
    Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr
     20          25          30
15  Asp Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val
     35          40          45
    Ala Ala Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val
     50          55          60
20  Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
     65          70          75          80
    Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys
     85          90          95
25  Gly Ala Gly Glu Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln
     100          105          110
30  Val Thr Val Ser Ser
     115

    <210> 25
35  <211> 43
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    <213> Artificial Sequence

    <220>
40  <223> Description of Artificial Sequence:PRIMER

    <400> 25
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45                                     43

    <210> 26
    <211> 42
    <212> DNA
    <213> Artificial Sequence

50  <220>
    <223> Description of Artificial Sequence:PRIMER

    <400> 26
55  ccctgggtcc agtggcagag gagtggcaga ggagtcttgt tt
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    <210> 27
    <211> 24
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Description of Artificial Sequence:PRIMER
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<400> 27
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5 <210> 28
 <211> 24
 <212> DNA
 <213> Artificial Sequence

10 <220>
 <223> Description of Artificial Sequence:PRIMER

<400> 28
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<210> 29
 <211> 55
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<220>
 <223> Description of Artificial Sequence:LINKER;DOUBLE
 25 STRANDED

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 <222> (2)..(40)
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 <222> (47)..(55)

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 Val Thr Val Ser Ser Gln Val Gln Leu Gln Glu Ser Xaa Xaa
 1 5 10

40 aag ctt 55
 Lys Leu
 15

45 <210> 30
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 <212> PRT
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 <223> Description of Artificial Sequence:LINKER;DOUBLE
 50 STRANDED

<400> 30
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 1 5 10

55

<210> 31
 <211> 3
 <212> PRT
 60 <213> Artificial Sequence
 <223> Description of Artificial Sequence:LINKER;DOUBLE
 STRANDED

<400> 31
 65 Xaa Lys Leu

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10

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1

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 <211> 672
 <212> DNA
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 <223> Description of Artificial Sequence: PLASMID
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 15 <220>
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 <222> (1)..(672)

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 20 1 5 10 15

 tcc tgt gca gcc tct gga cgc acc ggc agt acg tat gac atg ggc tgg 96
 Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr Asp Met Gly Trp
 25 20 25 30

 ttc cgc cag gct cca ggg aag gag cgt gag tct gta gca gct att aac 144
 Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val Ala Ala Ile Asn
 35 35 40 45

 30 tgg gat agt gcg cgc aca tac tat gca agc tcc gtg agg ggc cga ttc 192
 Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val Arg Gly Arg Phe
 50 55 60

 acc atc tcc aga gac aac gcc aag aag acg gtg tat ctg caa atg aac 240
 Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu Gln Met Asn
 35 65 70 75 80

 agc ctg aaa cct gag gac acg gcc gtt tat acc tgt ggc gcg ggg gaa 288
 Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys Gly Ala Gly Glu
 40 85 90 95

 ggt ggt act tgg gac tcc tgg ggc cag ggg acc cag gtc acc gtc tcc 336
 Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 45 100 105 110

 tca cag gtg cag ctg cag gag tca ggg gga ggc ttg gtg cag gct ggg 384
 Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 115 120 125

 50 gag tct ctg aaa ctc tcc tgt gca gcc tct gga aac acc ttc agt ggc 432
 Glu Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly
 130 135 140

 ggc ttc atg ggc tgg tac cgc cag gct cca ggg aag cag cgc gag ttg 480
 Gly Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu
 55 145 150 155 160

 gtc gca acc att aat agt aga ggt atc aca aac tat gca gac ttc gtg 528
 Val Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val
 60 165 170 175

 aag ggc cga ttc acc atc tcc aga gac aat gcc aag aag aca gtg tat 576
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
 180 185 190
 65

	ttg gaa atg aac agc ctg gaa cct gaa gac acg gcc gtt tat tac tgt	624
	Leu Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys	
	195 200 205	
5	tac act cac tac ttc aga tcc tac tgg ggt cag ggg acc cag gtc acc	672
	Tyr Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr	
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15	CONSTRUCT	
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20	Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr Asp Met Gly Trp	
	20 25 30	
25	Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val Ala Ala Ile Asn	
	35 40 45	
	Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val Arg Gly Arg Phe	
	50 55 60	
30	Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu Gln Met Asn	
	65 70 75 80	
	Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys Gly Ala Gly Glu	
	85 90 95	
35	Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln Val Thr Val Ser	
	100 105 110	
40	Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly	
	115 120 125	
	Glu Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly	
	130 135 140	
45	Gly Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu	
	145 150 155 160	
	Val Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val	
	165 170 175	
50	Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr	
	180 185 190	
55	Leu Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys	
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<220>
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5 <400> 34
 gtcacgctct ctagatggcc accaggtgca gctgcaggag tcaactta 48

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15 <220>
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35 <210> 37
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40 <220>
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45 <400> 37
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50 <210> 38
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50 <220>
 <223> Description of Artificial Sequence:LINKER

55 <400> 38
 ctagttcttc atctgcttct gcctcttcag ccag 35

60 <210> 39
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65 <220>
 <223> Description of Artificial Sequence:LINKER

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13

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<400> 39
aagaagtaga cgaagacgga gaagtcgg 28

5 <210> 40
<211> 29
<212> DNA
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10 <220>
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<400> 40
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20 <213> Artificial Sequence

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25 <400> 41
accaagaggt ccaagtggc ca 22

<210> 42
30 <211> 41
<212> DNA
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35 <223> Description of Artificial Sequence:LINKER

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55 <212> DNA
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65 <210> 45

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14

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<211> 25
<212> DNA
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5 <220>
<223> Description of Artificial Sequence:LINKER

10 <400> 45
acgattagta agaccattac gaaga

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